

SEQUENCE LISTING

<110> Steinkasserer, Alexander

<120> Use of Soluble Forms of CD83 and Nucleic Acids Encoding them for the Treatment or Prevention of Diseases

<130> 032723woJH

<140>

<141>

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 618

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> CBS

<400> 1

atg tcg cgc ggc ctc cag ctt ctg ctc ctg agc tgc gcc tac agc ctg
Met Ser Arg Gly Leu Gln Leu Leu Leu Ser Cys Ala Tyr Ser Leu
1 5 10 15

ttg ccc tgc acc gcc ccc tgg gat ccg cag gtt ccc tac acg gtc tcc 144
 Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
 35 40 45

tgg gtc aag tta ttg gag ggt ggt gaa gag agg atg gag aca ccc cag 192
Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
.....50.....55.....60.....

gaa gac cac ctc agg gga cag cac tat cat cag aag ggg caa aat ggt . 240
 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65 70 75 80

tct ttc gac gcc ccc aat gaa agg ccc tat tcc ctg aag atc cga aac 288
Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
85 90 95

act acc agc tgc aac tcg ggg aca tac agg tgc act ctg cag gac ccg 336
 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
 100 105 110

gat ggg cag aga aac cta agt ggc aag gtg atc ttg aga gtg aca gga 384
Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
115 . . . 120 . . . 125

tgc cct gca cag cgt aaa gaa gag act ttt aag aaa tac aga gcg gag 432
 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
 130 135 140

att gtc ctg ctg ctg gct ctg gtt att ttc tac tta aca ctc atc att 480
Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
145 . 150 155 160

ttc act tgt aag ttt gca cgg cta cag agt atc ttc cca gat ttt tct 528
 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
 165 170 175

aaa gct ggc atg gaa cga gct ttt ctc cca gtt acc tcc cca aat aag 576
 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
 180 185 190

cat tta ggg cta gtg act cct cac aag aca gaa ctg gta tga 618
 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
 195 200 205

<210> 2
<211> 205
<212> PRT
<213> Homo sapiens

<400> 2
Met Ser Arg Gly Leu Gln Leu Leu Leu Ser Cys Ala Tyr Ser Leu
 1 5 10 15

Ala Pro Ala Thr Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp
 20 25 30

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
 35 40 45

Trp Val Lys Leu Leu Glu Gly Glu Glu Arg Met Glu Thr Pro Gln
 50 55 60

Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65 70 75 80

Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
 85 90 95

Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
 100 105 110

Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
 115 120 125

Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
 130 135 140

Ile Val Leu Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
 145 150 155 160

Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
 165 170 175

Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
 180 185 190

His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
 195 200 205

<210> 3
<211> 2051
<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14)..(601)

<400> 3

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1 5 10	

gcc tgc agc ctg gca ccc gcg atg gcg atg cgg gag gtg acg gtg gct	97
Ala Cys Ser Leu Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala	
15 20 25	

tgc tcc gag acc gcc gac ttg cct tgc aca gcg ccc tgg gac ccg cag	145
Cys Ser Glu Thr Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln	
30 35 40	

ctc tcc tat gca gtg tcc tgg gcc aag gtc tcc gag agt ggc act gag	193
Leu Ser Tyr Ala Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu	
45 50 55 60	

agt gtg gag ctc ccg gag agc aag caa aac agc tcc ttc gag gcc ccc	241
Ser Val Glu Leu Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro	
65 70 75	

agg aga agg gcc tat tcc ctg acg atc caa aac act acc atc tgc agc	289
Arg Arg Arg Ala Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser	
80 85 90	

tcg ggc acc tac agg tgt gcc ctg cag gag ctc gga ggg cag cgc aac	337
Ser Gly Thr Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn	
95 100 105	

ttg agc ggc acc gtg gtt ctg aag gtg aca gga tgc ccc aag gaa gct	385
Leu Ser Gly Thr Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala	
110 115 120	

aca gag tca act ttc agg aag tac agg gca gaa gct gtg ttg ctc ttc	433
Thr Glu Ser Thr Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe	
125 130 135 140	

tct ctg gtt ttc tac ctg aca ctc atc att ttc acc tgc aaa ttt	481
Ser Leu Val Val Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe	
145 150 155	

gca cga cta caa agc att ttc cca gat att tct aaa cct ggt acg gaa	529
Ala Arg Leu Gln Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu	
160 165 170	

caa gct ttt ctt cca gtc acc tcc cca agc aaa cat ttg ggg cca gtg	577
Gln Ala Phe Leu Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val	
175 180 185	

acc ctt cct aag aca gaa acg gta tgtagtaggat ctccactggc ttttacaaag	631
Thr Leu Pro Lys Thr Glu Thr Val	
190 195	

ccaaggccac atcagatcag tgtgcctgaa tgccacccgg acaagagaag aatgagctcc 691

atcctcagat ggcaaccttt ctttgaagtc ctgcacactgaa cagtgccgtc cacactactc 751
cctgacacag ggtcttgagc accatcatat gatcacgaag catggagtat caccgcttct 811
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gacaggccaa gctgtgagcc agtggaaat atttagcaaa taatttccca gtgcgaaggt 1111
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taatgagctg ggctccctcc tcatttgctt cccaaagaga ttttgcctt ctaatggtgt 1951
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tcagccatga ctttcatgct attaaaagaa tgcattgtgaa 2051

<210> 4
<211> 196
<212> PRT
<213> *Mus musculus*

<400> 4

Met Ser Gln Gly Leu Gln Leu Leu Phe Leu Gly Cys Ala Cys Ser Leu
1 5 . 10 15

Ala Pro Ala Met Ala Met Arg Glu Val Thr Val Ala Cys Ser Glu Thr
20 25 30

Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu Ser Tyr Ala
35 40 45

Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
50 55 60

Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
65 70 75 80

Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
85 90 95

Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
100 105 110

Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
115 120 125

Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
130 135 140

Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
145 150 155 160

Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
165 170 175

Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
180 185 190

Thr Glu Thr Val
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<210> 5
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer for CD83ext

<400> 5
tccccccggga acgcccggagg tgaaggtggc t 31

<210> 6
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: primer for CD83ext

<400> 6
aattagaatt ctcaaatctc cgctctgtat t 31

<210> 7
<211> 435
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: partial
sequence of pGEX2ThCD83ext
<220>
<221> CDS

<222> (1)..(417)

<220>

<221> mat_peptide

<222> (28)..(417)

<400> 7

cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag	48		
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu			
-5	-1	1	5

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc	96	
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro		
10	15	20

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag	144	
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu		
25	30	35

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga	192		
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly			
40	45	50	55

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat	240	
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn		
60	65	70

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg	288	
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser		
75	80	85

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta	336	
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu		
90	95	100

agt ggc aag gtg atc ttg aga gtg aca gga tgc cct gca cag cgt aaa	384	
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys		
105	110	115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact	435	
Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile		
120	125	130

<210> 8

<211> 139

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: partial sequence of pGEX2ThCD83ext

<400> 8

Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu			
-5	-1	1	5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro		
10	15	20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu		
25	30	35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly			
40	45	50	55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Cys Pro Ala Gln Arg Lys
 105 110 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 9

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: partial
 sequence of pGEX2ThCD83ext_mut129_CtoS

<220>

<221> CDS

<222> (1)..(417)

<220>

<221> mat_peptide

<222> (28)..(417)

<400> 9

cct cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gga acg ccg gag	48
Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu	
-5 -1 1 5	

gtg aag gtg gct tgc tcc gaa gat gtg gac ttg ccc tgc acc gcc ccc	96
Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro	
10 15 20	

tgg gat ccg cag gtt ccc tac acg gtc tcc tgg gtc aag tta ttg gag	144
Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu	
25 30 35	

ggt ggt gaa gag agg atg gag aca ccc cag gaa gac cac ctc agg gga	192
Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly	
40 45 50 55	

cag cac tat cat cag aag ggg caa aat ggt tct ttc gac gcc ccc aat	240
Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn	
60 65 70	

gaa agg ccc tat tcc ctg aag atc cga aac act acc agc tgc aac tcg	288
Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser	
75 80 85	

ggg aca tac agg tgc act ctg cag gac ccg gat ggg cag aga aac cta	336
Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu	
90 95 100	

agt ggc aag gtg atc ttg aga gtg aca gga tcc cct gca cag cgt aaa	384
Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys	

105

110

115

gaa gag act ttt aag aaa tac aga gcg gag att tgagaattca tcgtgact 435
 Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 10

<211> 139

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: partial sequence of pGEX2ThCD83ext_mut129_CtoS

<400> 11

Pro Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Gly Thr Pro Glu
 -5 -1 1 5

Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr Ala Pro
 10 15 20

Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu Leu Glu
 25 30 35

Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu Arg Gly
 40 45 50 55

Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala Pro Asn
 60 65 70

Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys Asn Ser
 75 80 85

Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg Asn Leu
 90 95 100

Ser Gly Lys Val Ile Leu Arg Val Thr Gly Ser Pro Ala Gln Arg Lys
 105 110 115

Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu Ile
 120 125 130

<210> 11

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer sense-pGEX2ThCD83

<400> 11

tccccccggg aacgccggag gtgaagggtgg ct

32

<210> 12

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

antisense-CD83extra_mutantCtos

<400> 12
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ggggat 66